

FIGURE 5

1 ATGGAACCTG AGTGCCTCGG ACATCACCCG GGTCTCAAA CTCTACGGCT GCAGCCAAG
 w n l s a s d i t r v l k l y g c s p
 61 TGGCCCCAGG CCCCCGTGGGA GAGGGTCCCA TGCCCACAGC ACTGGTAGGA GCCCGCTCC
 s g p r p r g r g s h a h s t g r s p a
 121 GGCCTCCCTA TCTCTGCAGC GGCTTTGGA GGCACTGTCG CGGAAATCCA GGAGCCCCGA
 p a s l s l q r l l e a l s a e s r s p
 181 CCCCAGTGGT TCCAGTGCGG GAGGCCAGCC CGTTCCGTGCA GGGCCTGGGG AGAGCCCACA
 d p s g s s a g g q p v p a g p g e s p
 241 TGGGTGGGAG TCCCCTGCC TGAAAAAGCT CAGTGCAGAG GCCTCGGCAA GGCAGCCTCA
 h g w e s p a l k k l s a e a s a r q p
 301 GACCCTAGCT TCCTCCCCAA GATCAAGGCC TGGAGCAGGT GCCCCCGGTG TTGCTCAGGA
 q t l a s s p r s r p g a g a p g v a q
 361 GCAGTCCTGG CTGGCCGGAG TGTCCACCAA GCCCACAGTC CCATCTTCAG AAGCAGGAAT
 e q s w l a g v s t k p t v p s s e a g
 421 CCAGCCAGTC CCTGTCCAGG GAAGCCCAGC TCTGCCAGGG GGCTGTGTAC CTAGAAATCA
 i q p v p v q g s p a l p g g c v p r n
 481 TTTCAAGGGG ATGTCCGAAG ATTAAGCCTG TGGCTTCTGT CCCCAAGTAG GGAGGGCATC
 h f k g m s e d
 541 CTCTGCCAG TGGAGCTGGG TCGTCTACCT CTTGGCTCCT TTGGGCCACA CCACTGTCTT
 601 CCAGCCCCAA CCTACCACCC CATCTCAGAG GGCCAGGACT CTTCCCTGT CTCTCTTCAC
 661 TGTGTTCCCC TAAGGGCTCC TAGGCCAGG GTTCTTCTA GCTCTGCCAC AGGGGAAGGC
 721 AGGCCTGGCT GTGCCCTGCTC TTGACTTTG CCCAGCCCTG GTGGATGCTG GGAATGGGAG
 781 GTGACATTCT CCAGGGACAG GTCCTGGAAG GGGTGGGAA GAGGTAGGTT CCAGCCCCGC
 841 AGAACCTGG AATCCCTCCT GTGCCTGAGG CCCTGCCCTC CAGCATGGAC TAATGGTGT
 901 CCTACCTCTC CCTCAGGGCA GCCCTGTGGC TGGGACCTG GGAACAGCCT CCCATCCCAC
 961 CCAACATGCC CAAGTGTGGG GGAATGTTCT ACAGCAGTGT AGCCTCCAGC CCTTCTCTCC
 1021 AGGAGGCTT GAGAGCCAA CTTACTCCCC TGCAGAGCAG GAAGGTGGTA GGTCAAGTGT
 1081 GGCCACCATT GGGGAGACGA GAAAGAAGTG GGGCCCCACC AGATTGCACA ATGGGAACCT
 1141 CAGCTGGCC CTGAACAGAG GACTCAGTTG TCTCCACCT ACACCGCTAT TCCCTGGAGC
 1201 TCAGCCAGGC GCAGCCTTGG AAGGAGAAAG GGCTGGGTT ACCTGGCTTG TCCTCCTCCA
 1261 GGAAAGCCCC CTCCTCCCTC TGCCCCAGCT CCCAGCCTGG CCTCCCTCCAG GCAGGCCCTA
 1321 CTCCTCTGCC CCAGCTCCGG CTTTCCCCAT GAGGTTGTC CCAGGCATGA AGAAAGCATC
 1381 CAGGGTCCA ATGAGTGGGC CTAGGCCAGA GGCCCTCAG TCCCCAAGGG TACTGTTTG
 1441 GTGGCCTTTC AGAGGGTCAA GGAAGCCCTG CTTGGGGTAG AAGGGCAGG AGCCCCACAT
 1501 GTTGGGGAG GAAATAAAGT GGAGTGTGCT GTGCTGAAA AAAAAAAA AAAA

TAA Stop codon

AATAAA Consensus polyadenylation site (underlined)

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FIGURE 10 (continued)

1081 CTCGGCAAGG CAGCCTCAGA CCCTAGCTTC CTCCCCAAGA TCAAGGCCTG GAGCAGGTGC
a s a r q p q t l a s s p r s r p g a g
1141 CCCCGGTGTT GCTCAGGAGC AGTCCTGGCT GGCCGGAGTG TCCACCAAGC CCACAGTCCC
a p g v a q e q s w l a g v s t k p t v
1201 ATCTTCAGAA GCAGGAATCC AGCCAGTCCC TGTCCAGGGGA AGCCCAGCTC TGCCAGGGGG
p s s e a g i q p v p v q g s p a l p g
1261 CTGTGTACCT AGAAATCATT TCAAGGGGAT GTCCGAAGAT TAAGCCTGTG GCT
g c v p r n h f k g m s e d ←
78836-FL-R

FIGURE 13

Active site residues are underlined below.

WO2002/16566-A2	-----MEGVGGLWPVVLGLLSPGVILGAPLASSCAGACGTSFPDGLTPEGTQASGDKDI
AX526191	<u>MSCCLVSPVGAPGICVCPCLSGPGVILGAPLASSCAGACGTSFPDGLTPEGTQASGDKDI</u>
INSP005 PREDICTION	-----
INSP005b	-----MEGVGGLWPVVLGLLSPGVILGAPLASSCAGACGTSFPDGLTPEGTQASGDKDI
INSP005a	-----
WO2002/16566-A2	PAINQGLILEETPESSTFLIEGDIIRPSPFRLSATSNKWPMSGGVVEVPFLLSSKYDEP
AX526191	PAIN <u>QGLILEETPESSTFLIEGDIIRPSPFRLSATSNKWPMSGGVVEVPFLLSSKYDEP</u>
INSP005 PREDICTION	-----WPMGGSGVVEVPFLLSSKYDEP
INSP005b	PAIN <u>QGLILEETPESSTFLIEGDIIRPSPFRLSATSNKWPMSGGVVEVPFLLSSKYDEP</u>
INSP005a	-----MGGSGVVEVPFLLSSKYDEP

WO2002/16566-A2	SRQVILEALAEFERSTCIRFVTYQDQRDFISIIPMYGCFSSVGRSGMQVVSLAPTCLOK
AX526191	SRQVILEALAEFERSTCIRFVTYQDQRDFISIIPMYGCFSSVGRSGMQVVSLAPTCLOK
INSP005 PREDICTION	SHQVILEALAEFERSTCIRFVTYQDQRDFISIIPMYGCFSSVGRSGGMQVVSLAPTCLOK
INSP005b	SRQVILEALAEFERSTCIRFVTYQDQRDFISIIPMYGCFSSVGRSGGMQVVSLAPTCLOK
INSP005a	SRQVILEALAEFERSTCIRFVTYQDQRDFISIIPMYGCFSSVGRSGGMQVVSLAPTCLOK
	*:*****
WO2002/16566-A2	GRGIVL <u>HELMHVLGF</u> WHEHTRADRDYIRVNNEILPGFEINFIKSRSNNMLTPYDYSSV
AX526191	GRGIVL <u>HELMHVLGF</u> WHEHTRADRDYIRVNNEILPGFEINFIKSRSNNMLTPYDYSSV
INSP005 PREDICTION	GRGIVL <u>HELMHVLGF</u> WHEHTRADRDYIRVNNEILPGFEINFIKSQSSNNMLTPYDYSSV
INSP005b	GRGIVL <u>HELMHVLGF</u> WHEHTRADRDYIRVNNEILPGFEINFIKSRSNNMLTPYDYSSV
INSP005a	GRGIVL <u>HELMHVLGF</u> WHEHTRADRDYIRVNNEILPGFEINFIKSQSSNNMLTPYDYSSV
	*:*****;
WO2002/16566-A2	MHYGRLAFSRRGLPTITPLWAPS vhigqrwnlsasditrvlklygcspsgprprgrg ---
AX526191	MHYGRLAFSRRGLPTITPLWAPS vhigqrwnlsasditrvlklygcspsgprprgrg sha
INSP005 PREDICTION	MHYGRLAFSRRGLPTITPLWAPS vhigqrwnlsasditrvlklygc -----
INSP005b	MHYGRLAFSRRGLPTITPLWAPS vhigqrwnlsasditrvlklygcspsgprprgrg sha
INSP005a	MHYGRLAFSRRGLPTITPLWAPS vhigqrwnlsasditrvlklygcspsgprprgrg sha
	*:*****:.: . . . :

FIGURE 13 (continued)